

STIC-Biot ch/ChemLib

83130

From: Li, Ruixiang
Sent: Friday, December 27, 2002 2:28 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application NO: 09/898,586

Please do a standard search on SEQ ID NO: 24 against interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10E18
Mail Box 10D19
306-0282

Point of Contact:
Toby Fort
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/2
Date Completed: 1/9
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Alignment Scores:
Pred. No.: 2.02e-142 Length: 974
Score: 1609.00 Matches: 310
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 38 Gaps: 0

US-09-898-586-24 (1-310) x

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QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
DB 361 CTGTAGCTGGCCATGCTGCCACCCCTCCGATATTGGCCATGACCTGAGAGCTGCG 420
QY 141 IleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
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DB 481 TTACTTCTACCTTTACCTCTCTGTAGGCCCCAGAAATTATCAGCTTTTGTGTAATC 540
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
DB 541 TTGGCTCTCTCAAACTGCTGTCGACATACCCACATCAATGAGACATGCTGTGGCC 600
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QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
DB 721 TTCTCCACCTCTGTGTGATTTGACTCTTTTATGGCAGCCATTAATGATGTTGA 780
QY 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
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QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
DB 841 AATCCCATGCTCAATCCCTTATCTGTAGTCTTAGAACTCAGAAAGTGAAGATACTTTG 900
QY 301 LysArgValLeuGlyValGluArgAlaLeu 310
DB 901 AAGAGAGTCTGCTGAGGAGTGAAGAGGCTTTTA 930

ALIGNMENTS

RESULT 1

Sequence 41, [REDACTED]
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: AU-YOUNG, Janice
APPLICANT: BANDMAN, Olga
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: BURFORD, Neil
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dzung Alina M.
APPLICANT: HILMAN, Jennifer L.
APPLICANT: PATTERSON, Chandra
APPLICANT: LAL, Preeti
TITLE OF INVENTION: RECEPTORS AND ASSOCIATED PROTEINS
FILE REFERENCE: PF-0726 PCT
PRIOR APPLICATION NUMBER: 60/145,232; 60/158,578; 60/165,192
PRIOR FILING DATE: 1999-07-21; 1999-10-07; 1999-11-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
SEQ ID NO 41
LENGTH: 974
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 2, 2003, 08:42:37 ; Search time 77 Seconds
(without alignments)
1234.673 Million cell updates/sec

Title: US-09-898-586-24

Perfect score: 1609

Sequence: 1 MCDNITSIFELLGFPVGP.....LRNSEVKNLTKRVLGVERAL 310

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048.5	65.2	1713	2	US-08-467-948A-1 Sequence 1, Appl1
2	1048.5	65.2	1713	3	US-08-467-947A-1 Sequence 1, Appl1
3	609	37.8	966	3	US-08-748-506-5 Sequence 5, Appl1
4	606	37.7	1290	2	US-08-827-291A-1 Sequence 1, Appl1
5	605	37.6	1062	4	US-09-668-680-10 Sequence 10, Appl1
6	592	36.8	966	3	US-08-748-506-7 Sequence 7, Appl1
7	578	35.9	966	3	US-08-748-506-8 Sequence 8, Appl1
8	574	35.7	966	3	US-08-748-506-6 Sequence 6, Appl1
9	543	33.7	900	4	US-09-085-371-5 Sequence 5, Appl1
10	524	32.6	1297	4	US-09-668-680-11 Sequence 11, Appl1
11	521	32.4	1080	4	US-09-668-680-9 Sequence 9, Appl1
12	452	28.1	984	3	US-08-748-506-9 Sequence 9, Appl1

13	418.5	26.0	1539	4	US-09-668-680-13 Sequence 13, Appl1
14	384	23.9	963	4	US-09-605-785-526 Sequence 526, App
15	384	23.9	963	4	US-09-439-313-526 Sequence 526, App
16	382.5	23.8	1828	3	US-08-988-876-2 Sequence 2, Appl1
17	369	22.9	1474	1	US-08-465-980-1 Sequence 1, Appl1
18	369	22.9	1474	2	US-09-053-303-1 Sequence 1, Appl1
19	369	22.9	1474	4	US-09-339-115-1 Sequence 1, Appl1
20	369	22.9	1474	5	PCT-US95-07093-1 Sequence 1, Appl1
21	236	14.7	897	4	US-09-668-680-5 Sequence 17, Appl1
22	185.5	11.5	978	3	US-08-706-281A-17 Sequence 17, Appl1
23	185.5	11.5	978	4	US-09-097-231-17 Sequence 17, Appl1
24	182.5	11.3	975	1	US-08-671-525B-9 Sequence 9, Appl1
25	182.5	11.3	975	1	US-08-672-109B-9 Sequence 9, Appl1
26	182.5	11.3	975	1	US-08-842-045-9 Sequence 9, Appl1
27	182.5	11.3	975	2	US-08-842-238-9 Sequence 9, Appl1
28	182.5	11.3	975	3	US-08-629-335B-9 Sequence 9, Appl1
29	181	11.2	1320	1	US-08-599-252-84 Sequence 84, Appl1
30	181	11.2	1320	1	US-08-436-074-57 Sequence 57, Appl1
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33	179.5	11.2	1650	4	US-08-387-805-15 Sequence 15, Appl1
34	175	10.9	999	4	US-08-870-511-7 Sequence 7, Appl1
35	174.5	10.8	1080	1	US-08-671-525B-5 Sequence 5, Appl1
36	174.5	10.8	1080	1	US-08-672-109B-5 Sequence 5, Appl1
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40	173	10.8	996	1	US-08-671-525B-7 Sequence 7, Appl1
41	173	10.8	996	1	US-08-842-045-7 Sequence 7, Appl1
42	173	10.8	996	1	US-08-842-238-7 Sequence 7, Appl1
43	173	10.8	996	2	US-08-842-238-7 Sequence 7, Appl1
44	173	10.8	996	3	US-08-629-335B-7 Sequence 7, Appl1
45	173	10.8	999	4	US-08-870-511-9 Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-467-948A-1
; Sequence 1, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULL, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCE: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.,
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467, 948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.

Db 328 TTGCGATTTTGGTATAACTGAGTGCTGCCCTATTTGGCAGCCATGGCCTTTGACCGCTGC 387
OY 123 ValAlaIleCysHisProLeuArgPheLeuAlaIleMetThrTrpArgValCysIleThr 142
Db 388 ATGGCCATATGCTCCCTGACCTCAGATGCAACCCGAATGAGTGCNGAGGTATGTGCCAT 447
OY 143 LeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 162
Db 448 TTGGCAATGTTTCATGGGGAATGGGATGCATAGTAAGTCTGGGACAAACCAATTTTATT 507
OY 163 LeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAla 182
Db 508 TTCTCCTGAACTTCTGTGGACCCCTGTGAATAGACCACCTTCTGTGACCTTCCACCT 567
OY 183 ValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAla 202
Db 568 CTCTGACACTGCTGCTGTGAGATACATCCCAAAACGAGGCTGCCATCTTTGTGGTAGCA 627
OY 203 IleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCys 222
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Db 688 GCAGTGCTNCTGATGCCCTTCACCTGAGGGGGGCCCATTAAGCTCTTCCACCTGTTCGCTCT 747
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OY 263 TyrGlyAsnProLysGluGlnLysTyrLeuLeuPheHisSerLeuPheAsnPro 282
Db 808 TCTAGCCACTGCACCAAGAAAGCAAAATCTTGGCCCTCTTCTACACAGTAGACATGCC 867
OY 283 MetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArg 302
Db 868 ATGCTGAACCTATATCATCTATAGTTTAAGGAACAMGGAAGTCAAGGACACTGAGAAAGA 927
OY 303 ValLeuGlyValGluArgAlaLeu 310
Db 928 ACTCTGGGCTGAAAAAATTTCTG 951
RESULT 4
; Sequence 1, Application US/08827291A
; Patent No. 5874243
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Sathe, Ganesh
; TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: PA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,291A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954

REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-827-291A-1
Alignment Scores:
Pred. No.: 1.33e-60 Length: 1290
Score: 606.00 Matches: 122
Percent Similarity: 59.87% Conservative: 60
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Query Match: 37.66% Indels: 2
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Cb 365 CACACCTTCCCTCTCTCTCTGTCCTGTCCTGCGCATCTTTTCAGTG--GCCTCATGGGAAC 421
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OY 102 LeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAspLeu 121
Db 602 TTCTATACATCAGCTGTGCTGTGAATGCTTTTGGCTGTGTATGGCTTATGACCGC 661
OY 122 TyrValAlaIleCysHisProLeuArgTyrIleAlaIleMetThrTrpArgValCysIle 141
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OY 142 ThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuValLeu 161
Db 722 CTTATGACTGCTTTTCTGTGATCTCTGGGCTCTACAGATGGAATCATTTATGCTGTAGCC 781
OY 162 LeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeu 181
Db 782 ACATTTTCCCTTCTCTACTGTGGGTCTCGGGAATAGCCCACTTCTGTGAGTTACCT 841
OY 182 AlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGly 201
Db 842 TCCTACTAATCCTCTCATGCAATGACACATCAATATTGAAAAGGTATTTTCATTTGC 901
OY 202 AlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeu 221
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Db 1082 ACATCTGATGCTCCCAACGACAGCAAGCTGGTGTCTGTATTTCTACACCATCTCCTCACT 1141
QY 282 PrometLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLys 301
Db 1142 CCCATGCTGAATCCCTCATCTACAGCTCCGCAACAAGAGTGAACGAGCATTTCAATG 1201
QY 302 ArgValLeuGly 305
Db 1202 AAGATCTCAGGA 1213

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RESULT 5
US-09-668-680-10
Sequence 10, Application US/09668680
Patent No. 6436703

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668, 680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: pt_fl_genes Version 2.0
SEQ ID NO 10
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1062)
-09-668-680-10

Alignment Scores:
Pred. NO.: 1.29e-60 Length: 1062
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Best Local Similarity: 41.58% Mismatches: 114
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US-09-898-586-24 (1-310) x US-09-668-680-10 (1-1062)

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Db 196 CCGTTCATATTGGGCTGTCTCTGCATGTACCTGGGAGCGTGTGGAAACCTGCTC 255
QY 44 IleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhePheLeuSer 63
Db 256 ATCATCTCGGCATCAGCTCTGACTCCACCTCCACACCCCATGTACTTCTCTCTCC 315
QY 64 HisLeuAlaValAlaSpIleAlaTyrAlaCysAsnThrValProArgMetLeuValAsn 83

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Db 316 AACCTGCTCGGGTGTGACATCTGTTTCAGCACTTGCATCGTCCCCAAGATGCTGTGAAC 375
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Db 376 ATCCAGACCCGAGAACAGCCATCTCCTACATGAGACTGCCCTCACACAGGTCTATTCTCC 435
QY 104 SerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAspLeuTyrVal 123
Db 436 ATGTTTTCCTATTTCTGTGACACGCTACTCTGACCGGTGATGGCCATGACCGGTTGTG 495
QY 124 AlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThrLeu 143
Db 496 GGTGTCGCCACCCCTGTGCACTATATGATCATCATGAACCCACCCCTGTGGCTCCTG 555
QY 144 AlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeuLeu 163
Db 556 GTTTTTCACCTGGCTCATTTGGTGTGATGACATCCCTCCATATTTCCTGATGATG 615
QY 164 ProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAlaVal 183
Db 616 CATCTAATCTTCTGTAAAGATTTTGAATTCACATTTTCTGCGAAGTGAACGTACATC 675
QY 184 LeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAlaGlyAlaIle 203
Db 676 CTCACAGCTGGCCTGCTGTGATACCTTCCCTGAACAGCAGTGTATATAC-----TTTATG 729
QY 204 SerGlyLeuValGly-----ProLeuSerThrIleValValSerTyrMetCysIleLeu 221
Db 730 ACGGCTGTGCTGGCGGCTTTTCCCTCCTGCGATCATTTTCTCTTATTCAGGAATTTGCT 789
QY 222 CysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPhe 241
Db 790 TCATCCATTAAGGAAGATGTCTCATCTGCGGGGAAACAAAGCACTTTCACCTGTGGG 849
QY 242 SerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyPro 261
Db 850 TCTCACCCTCTCCGTCGTTCTTATTATTATTTATGGACAGGCAFTGGGTCACCTTCTCT 909
QY 262 ArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPheAsn 281
Db 910 GCGGTGACTCACTCTTCCAGAAATCTCCGTGGCTGGTGATGTACACTGTGTCACC 969
QY 282 PrometLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLys 301
Db 970 CCCATGTTGAACCCCTTCATCTACAGCCTGAGGAACAAGATGTGAAGGAGAGCCCTGGGG 1029
QY 302 ArgValLeu 304
Db 1030 AGTCTCTC 1038

```

RESULT 6
US-08-748-506-7
Sequence 7, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748, 506
FILING DATE: 08-NOV-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-7

Alignment Scores:
Pred. No.: 3.55e-59 Length: 966
Score: 592.00 Matches: 124
Percent Similarity: 56.82% Conservative: 51
Best Local Similarity: 40.26% Mismatches: 133
Query Match: 36.79% Indels: 0
DB: 3 Gaps: 0

US-09-898-586-24 (1-310) x US-08-748-506-7 (1-966)

QY 3 AspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIle 22
DB 28 GAGAAATAGTTTGTCTGTCACAAACGCTTTCATTTGCCAAGTCTCTGAGGTCCTGGAGAA 87
QY 23 GluMetLeuLeuPheGlyLeuPheSerLeuPheThrValPheThrLeuLeuGlyAsnGly 42
DB 88 TGCTTCCTCCTGTCACCCCTCATCTCTCTCATGTTCTTAGTATACACTAACAGGAATACT 147
QY 43 ThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetIlePhePheLeu 62
DB 148 CTCATAGCCCTTGCTATTGTGTACCCAGTCCATCTCTACACACCCCATGTACTTCTTCG 207
QY 63 SerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeuVal 82
DB 208 GCCAACCTGTCTCTCTGAGATTGGCTATACTTCTCTGTATACCCAGATGCTGCAG 267
QY 83 AsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeu 102
DB 268 AGCCTGTGAGTGAGGCCCGCAGGAGTCTCTGGGAGGCTTGCCCTACAGATGTCTTC 327
QY 103 PheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAspLeuTyr 122
DB 328 TTCATATTCTTTGGTATACCTAGTGTGCTGCTATGGCAGCCATGGCCTTGGACCGCTAT 387
QY 123 ValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThr 142
DB 388 ATGGCTATATGTTCCCACTCCACATATGCAACCCGAATGAGTGGGTATGTCCTAT 447
QY 143 LeuAlaValThrSerThrThrThrGlyValLeuLeuSerLeuIleHisLeuValLeu 162
DB 448 TTGGCAATGTCTCATGGTGAATGGGATGCATAGTAGTCTGGGACAGACCAATTTTATT 507
QY 163 LeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAla 182
DB 508 TTCTCCTTGAACCTTCTGTGACCCCTGTGAGATAGACCACTTCTTGTGACCTTCACCT 567
QY 183 ValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAla 202
DB 568 CTCCTGGCACTTGCTGTGTGATACATCCCAAAATGAGGCTGCCATCTTGTGGCAGCA 627
QY 203 IleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCys 222
DB 628 GTGCTGTGCATATTAGTCCATTTTACTGATCATTTCTTCCTATGTGAGAAATTCCTGTT 687

QY 223 AlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSer 242
DB 688 GCAGTGTGTGATGCTTCACCTGAGGGGGCCCATAAAGCTCTCTACCTGTTCATCT 747
QY 243 HisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArg 262
DB 748 CACCTACTGTGTACACTCTCTCTATGCTCAACATCTGCCACCTATTGTGAGTCCAAAG 807
QY 263 TyrGlyAsnProLysGluGlnLysIleTyrLeuLeuPheHisSerLeuPheAsnPro 282
DB 808 TCTAGCCACTCACCGAGAGTGGACAACCTTGGCCCTCTTCTATACATCAGTGACATCC 867
QY 283 MetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArg 302
DB 868 ATGCTGAATCCCATCATCTACAGCTTAAGGACAAGAAAGTAAGGCTGACACTGAGAAAGA 927
QY 303 ValLeuGlyValGluArgAlaLeu 310
DB 928 ACTCTGGCCCTGAAGAAAGTCTCTG 951

RESULT 7

US-08-748-506-8
Sequence 8, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Konnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL

COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-8

Alignment Scores:

Pred. No.: 1.48e-57 Length: 966
Score: 578.00 Matches: 120
Percent Similarity: 56.17% Conservative: 53
Best Local Similarity: 38.96% Mismatches: 135
Query Match: 35.92% Indels: 0
DB: 3 Gaps: 0

US-09-898-586-24 (1-310) x US-08-748-506-8 (1-966)

QY 3 AspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIle 22

DB 28 GAGAAATAGTTGTCTGTCAACCGTTTTCATTTGCCAGTTCTCTGAGGTCCTGGAGAA 87
QY 23 GlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGlyAsnGly 42
DB 88 TGCTTCCTCTGTTCCACCCCTCACTCTTCTCATGTGTAGTATCAGTAACAGGAATGCT 147
QY 43 ThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhePheLeu 62
DB 148 CTCATAGCCCTTGCTATTGTGACAGTCCATCTCTACACACCCCATGTACTCTTCTG 207
QY 63 SerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeuVal 82
DB 208 GCCAAGCTTGCTCTCTGAGATGGCTATACTTGTCTGTCAATACCCAGATGCTGCAG 267
QY 83 AsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeu 102
DB 268 AGTCTGTGAGTGAGGCCGAGAGATCTTTCAGGTGGAGTGTGCCACACAGATGTTTTC 327
QY 103 PheSerThrPheAlaValThrGlyCysLeuLeuValValMetSerTyrAspLeuTyr 122
DB 328 TTCATATCTTGTGGATAACTAGAGTGTGCTATTTGGACGCAATGGCTTGGACGCTAT 387
QY 123 ValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThr 142
DB 388 ATGGCTATATGTCCCACTCCACATATGCAACCCGAATGATGCTGAGTATGCCCCAC 447
QY 143 LeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 162
DB 448 TTGGCAATGTGTTCATGGGTGATGGATGCATAGTAGTGTGGGACAGACCAATTTTAT 507
QY 163 LeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAla 182
DB 508 TTCTCCTGCACTCTGTGAGCCCTGTGAGATGACACCACTTCTGTGATCTTCACCT 567
QY 183 ValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAla 202
DB 568 CTCCTGGCACTGCTGCTGTGATACATCCCAATTGAGGCTGCCATCTTGTGTAGTT 627
QY 203 IleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCys 222
DB 628 GTCTCTGCATATCTAGCCCTTTTCTGATCATTTATTTATGTCAGAATTCCTGCT 687
QY 223 AlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSer 242
DB 688 GCAGTGTGTGATGCTTCAACCTGAGGGGCGCCACAAAGCCCTTCAACCTGTTCCTCC 747
QY 243 HisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArg 262
DB 748 CACCTACTGTAGTACACACTTTTATGGCTCAGGATCTGTACCTATTGGAGCCCTAG 807
QY 263 TyrGlyAsnProLysGluGlnLysTyrLeuLeuPheHisSerLeuPheAsnPro 282
DB 808 TCTAGCCACTCAGCAGGAATGAGCAAACTTGGCCCTCTTCTACACAGCAGTGCATCC 867
QY 283 MetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArg 302
DB 868 ATGTTGAACCCCTATCATCTATAGTTTAAAGGAACAAGATGTCAAGGACGACTGAGA 927
QY 303 ValLeuGlyValGluArgAlaLeu 310
DB 928 ATTCTGGCCCTGAATAATTCTG 951

RESULT 8
US-08-748-506-6
; Sequence 6, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.

STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6
Alignment Scores:
Pred. No.: 4,3e-57 Length: 966
Score: 574.00 Matches: 121
Percent Similarity: 55.84% Conservative: 51
Best Local Similarity: 39,29% Mismatches: 136
Query Match: 35,67% Indels: 0
Gaps: 0
US-09-898-586-24 (1-310) x US-08-748-506-6 (1-966)
QY 3 AspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIle 22
DB 28 GAGAAATAGTTGTCTGTCAACCGTTTTCATTTGCCAGTTCTCTGAGGTCCTGGAGAA 87
QY 23 GlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGlyAsnGly 42
DB 88 TGCTTCCTCTGTTCCACCCCTCACTCTTCTCATGTGTAGTATCAGTAACAGGAATGCT 147
QY 43 ThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhePheLeu 62
DB 148 CTCATAGCCCTTGCTATTGTGACAGTCCATCTCTACACACCCCATGTACTCTTCTG 207
QY 63 SerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeuVal 82
DB 208 GCCAAGCTTGCTCTCTGAGATGGCTATACTTGTCTGTCAATACCCAGATGCTGCAG 267
QY 83 AsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeu 102
DB 268 AGCCTGTGAGTGAGGCCAGAGAGATCTCTAGGAGGAGATGTGCCACACAGATGTTTTC 327
QY 103 PheSerThrPheAlaValThrGlyCysLeuLeuValValMetSerTyrAspLeuTyr 122
DB 328 TTCATATCTTGTGGATAACTAGAGTGTGCTATTTGGACGCAATGGCTTGGACGCTAT 387
QY 123 ValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThr 142
DB 388 ATGGCAATATGCTCCCACTCCACATATGCAACCCGAATGATGCTGAGGATGTGCCAT 447
QY 143 LeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 162
DB 448 TTGGCAATGTGTTCATGGGATGGGATGCATAGTAGTGTGGGACAGACCAATTTTAT 507

OY 163 LeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAla 182
Db 508 TNCCTCTGAACCTCTGTGACCTTGTGAGATAGACCACTTCTTGTGACCTTCCACCT 567
OY 183 ValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAla 202
Db 568 CTCCTGGCACTTGCCTGTGGTATACATCCCAAAACGAGGCTGCCATCTTGTGGCAGCA 627
OY 203 IleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCys 222
Db 628 ATCCTCTGTATATCTAGTCCATTTTGGTGATCCTTTATTTATGTACAGATTCTCGTT 687
OY 223 AlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSer 242
Db 688 GCAGTCTGTGATGCCCTTACCTGAGGGGGCCCATTAAGCTCTTCCACCTGTCTCTCA 747
OY 243 HisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArg 262
Db 748 CACCTACTGTAGTCAACACTCTTTTATGGCTCTGTCTCTTACCTATTGTAGGCCCAAG 807
OY 263 TyrGlyAsnProLysGluGlnLysLysTyrLeuLeuPheHisSerLeuPheAsnPro 282
Db 808 TCTAGCCACTCACCAGAAATGACAAACCTTGGCCCTCTTACACAGCAGTGACATCC 867
OY 283 MetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArg 302
Db 868 ATGCTGAACCTTATCATCTACAGTTAAGGAACAAGAAAGTCAAGGCACGACTGAGAAGA 927
OY 303 ValLeuGlyValGluArgAlaLeu 310
Db 928 ACTCTCGACCTGAATAAATTATG 951

RESULT 9
US-09-085-371-5
; Sequence 5, Application US/09085371
; Patent No. 6218358
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; APPLICANT: Zhao, Haiqing
; TITLE OF INVENTION: Functional Expression of, and Assay for, Functional Cellular Re
; FILE REFERENCE: P0151IUS2 / 09805059
; CURRENT APPLICATION NUMBER: US/09/085,371
; CURRENT FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: US 08/891,243
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: US 60/045,961
; PRIOR FILING DATE: 1997-05-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Rat
US-09-085-371-5

Alignment Scores:
Pred. No.: 1.49e-53 Length: 900
Score: 543.00 Matches: 114
Percent Similarity: 58.28% Conservative: 55
Best Local Similarity: 39.31% Mismatches: 117
Query Match: 33.75% Indels: 4
DB: 4 Gaps: 1

US-09-898-586-24 (1-310) x US-09-085-371-5 (1-900)

OY 8 IleThrGluPheLeuLeuLeuGlyPheProValGlyProArgIleGlnMetLeuPhe 27
Db 28 GTGAGTGAATTGTGTGCTGGTTCACAGCTCCTGCCCACTGCGAGTACTATT 87
OY 28 GlyLeuPheSerLeuPheTyrValPheThrLeuLeuGlyAsnGlyThrIleLeuGlyLeu 47

Db 88 TTCCTTCTCTCTGAGCTATAGTGTGGTGTGACTGAAACATGCTCATCTATAGCA 147
OY 48 IleSerLeuAspSerArgLysHisAlaProMetTyrPhePheLeuSerHisLeuAlaVal 67
Db 148 ATTAGGAACCAACCAACCCCTCCACAAACCATGATTTTCTTGGCTAATATGTCATTT 207
OY 68 ValAspIleAlaTyrAlaCysAsnThrValProArgMetLeuValAsnLeuLeu----- 85
Db 208 CTGAGATTGGTATGTCACTGTTCAGATTCTTAAGATGCTCGCTGGCTTCATTGGTTCC 267
CY 86 -----HisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeuPhe 103
Db 268 AAGGAGAACCATGGACAGCTGATCTCTTGAAGGCATGCATGACACAACTCTACTTTTTC 327
CY 104 SerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAspLeuTyrVal 123
Db 328 CTGGGCTTGGTGGACAGAGTGTGCTCTTGTGCTGTGATGGCCATGACCCCTATGTG 387
CY 124 AlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThrLeu 143
Db 388 GCTATCTGTCACTCACCTCCACTACCCCGTCAATGTCAAGTACCCGGCTATGTGAGATG 447
CY 144 AlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 163
Db 448 GCAGCTGCATCCTGGGCTGGAGGTTTGGTATCTTCATGTTAAAGTTTTCCTTATTTCT 507
CY 164 ProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIleLeuAlaVal 183
Db 508 CGCTGTCTTACTGTGGCCCAACACACATCAACCACTTTTCTGTGATGTCTCCATTG 567
CY 184 LeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAlaIle 203
Db 568 CTCACCTGTGATGACACTGACATGTCCACAGCAGAGCTTACAGACTTGTCTGGCCATF 627
CY 204 SerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCysAla 223
Db 628 TTTATCTCTGCTGGACCGCTCTGTCTGCTGCTGGGCGCATCTTACATGCGCATACAGTGTCT 687
OY 224 IleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSerHis 243
Db 688 GTGATGGCATCCCTCAGCTGCTGGCCGCCATTAAGCTTTTCAACCTGTGCCCTCCAC 747
OY 244 LeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyr 263
Db 748 CTCACGTGTGTGATCATCTTCTATGCCAGCCAGTATTTCATCTATGCGAGGCTAAGGCA 807
CY 264 GlyAsnProLysGluGlnLysLysTyrLeuLeuPheHisSerLeuPheAsnProMet 283
Db 808 CTCCTCAGCTTTTGACACCAACAAGCTGGTCTGTACTGTACGCTGTCAATTGTACCGTTG 867
CY 284 LeuAsnProLeuIleCysSerLeuArgAsn 293
Db 868 TTCAATCCATCATCTACTGTGGCAAC 897

RESULT 10
US-09-668-680-11
; Sequence 11, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22


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; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 11
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1091)
US-09-668-680-11

Alignment Scores:
Pred. No.: 4.11e-51 Length: 1297
Score: 524.00 Matches: 116
Percent Similarity: 60.98% Conservative: 59
Best Local Similarity: 40.42% Mismatches: 110
Query Match: 32.57% Indels: 2
DB: 4 Gaps: 2

US-09-898-586-24 (1-310) x US-09-668-680-11 (1-1297)
QY 20 ProArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeu 39
   |||:::||||:::|||||
Db 186 CCAGAACTGGAGCGAGTCTGCTGGGCTGTCTCGCATGTGCTGTGCTGTCACGGTCTG 245
QY 40 GlyAsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyr 59
   |||||  |||:::  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 246 GGGAACCTGGCTCATCATCTCGGCCATCAGCCCTGACTCCACCTCCACACCCCGCTGAC 305
QY 60 PhePheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArg 79
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 306 TTCTTCCTTCACCAACTGTCTGCTGGCTGACATCGGTTTCACCTCCACCGGTCGCCAAG 365
QY 80 MetLeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGln 99
   |||:::||||:::  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 366 ATGATGTGGACATGCAAACTCAGCAGAGATCATCTCTGATGAAGGCTGCCTGACTCAG 425
QY 100 ThrPheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyr 119
   |||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 426 ATGCTTTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 485
QY 120 AspleuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgVal 139
   |||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 486 GACCGGTTTGGGCGCATCTGTACACCCCTGCACACTACCGAATCATGTAACCCGCGCTC 545
QY 140 CysIleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeu 159
   |||  |||  |||  |||||  |||||  |||||  |||||  |||||  |||||
Db 546 TGTGGCTTCCTAATCTGTGTCTTTTATATAGTCTTTTGGACTCCGAGTTGCACAAT 605
QY 160 ValLeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGlu 179
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 606 TTGATATATGTACAGCTCACCCTGCCTCAAGGATGTGGACATTTCTAATTTCTTCGTGAC 665
QY 180 IleLeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetVal--- 198
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 666 CCTTCTCAACTCCTCCACCTTAGGTTCCGACACCTTCATCAATGAATGTCATATAT 725
QY 199 LeuAlaGlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMet 218
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 726 TTCATGGGTGCATATTTGGCTGTCTC---CCTATCTCAGGAGTCTTCTCTTACTAT 782
QY 219 CysIleLeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCys 238
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 783 AAAATGTGTTCCCCCATTTCTGAGAGTTCCACACATCAGATGGGAGTATAAGCCCTTCTCC 842
QY 239 ThrCysPheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyr 258
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 843 ACCTGTGGCTCTACCTGGCAGAGTGTGCTTCTTATTTATGGAACAGGGCTTGTAGGGTAC 902
```

```
QY 259 ValGlyProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSer 278
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 903 CTCAGTTTCAGCTGTGTATACCATCCCCCAGAGAGATATGTTGGCTTCAGTGTACACT 962
QY 279 LeuPheAsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsn 298
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 963 GTGGTCACCCCATGCTGAACCCCTTCATCTACAGCCCTGAGGACACAGACATTCAAAGT 1022
QY 299 ThrLeuLysArgValLeuGly 305
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1023 GCCCTGTGCAGGCTGCATGGC 1043

RESULT 11
US-09-668-680-9
; Sequence 9, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (178)..(1080)
US-09-668-680-9

Alignment Scores:
Pred. No.: 6.91e-51 Length: 1080
Score: 521.00 Matches: 118
Percent Similarity: 58.67% Conservative: 58
Best Local Similarity: 39.33% Mismatches: 124
Query Match: 32.36% Indels: 0
DB: 4 Gaps: 0

US-09-898-586-24 (1-310) x US-09-668-680-9 (1-1080)
QY 4 AsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIleGln 23
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 91 AATCTGCACAGTATCTCAGAAATCTCTCTCGGACTCTCAGAGATCCAGAACTGCAG 150
QY 24 MetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGlyAsnGlyThr 43
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 151 CCCGTCTCCCTGGGCTGTCCCTGTCCATGTACCTGGTCACGGTGTGAGGAACCTGCTC 210
QY 44 IleuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhePheLeuSer 63
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 211 ATCATCTGGCTGTGAGCTGTGACTCCACCTGCACACCCCATGTGCTTCTCTCTCC 270
QY 64 HisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeuValAsn 83
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 271 AACCTGTGCTGGCTGACATCGGTTTCACCTCGGCCATGTGTCCCAAGATGATGTGAC 330
QY 84 LeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeuPhe 103
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```
Db 331 ATGCAGTCGCATAGCAGATCATCTTATGCGGGCTGCCGACACAGATGCTTCTTT 390
QY 104 SerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAspLeuTyrVal 123
Db 391 GTCCTTTTGCATGATAGACACATGCTCCTGACAGTATGACCTATGACCATTTGTG 450
QY 124 AlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThrLeu 143
Db 451 GCCATCTGTACACCCCTGCACCTACCATCATGAAATCCTCACCTGTGCTCTTCTTA 510
QY 144 AlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 163
Db 511 GTTTGGTGTCCCTTTTCCAGCCTGTGGATGCCAGTCACAGTTGGATTTGTTA 570
QY 164 ProLeuProPheCysArgProGlnIleTyrHisPhePheCysGluIleLeuAlaVal 183
Db 571 CAATTCACCTTCTTCAAGAAATGGAATCTCCAATTTTGTCTGTGACCCATCTCACTT 630
QY 184 LeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAlaIle 203
Db 631 CTCACCTTTCCTGCTGTGACAGTGCATCAATAGCATATATATTAGATAGTATT 690
QY 204 SerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCysAla 223
Db 691 ATGTTGGTTTCTTCCCATTTTCAGGAGATCCTTTGTCTTACGCTAACACATGTCCCTCC 750
QY 224 IleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSerHis 243
Db 751 ATCTAAGAAATTTTCATCATCATCAGATAGGAAGTCTAAAGCCTTCTCCACCTGTGGCTCTCAC 810
QY 244 LeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyr 263
Db 811 CTGGCAGTGTGCTTATTTATGGAACAGGACATTGGCGTGTACCTGACTTCAGCTGTG 870
QY 264 GlyAsnProLysGluGlnLysLysTyrLeuLeuPheHisSerLeuPheAsnProMet 283
Db 871 TCACACACCCCGAAGATGTGTGTGGCATCAGTATGATGACGCTGTGTCACCCCATG 930
QY 284 LeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgVal 303
Db 931 CTGAACCTTTCATCTACAGCCTGAGAAATAGGACATTCMAAGTCCCTGTGAGGCTG 990

RESULT 12
US-08-748-506-9
; Sequence 9, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Romnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748, 506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
```

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-9

Alignment Scores:
Pred. No.: 5.78e-43 Length: 984
Score: 452.00 Matches: 97
Percent Similarity: 52.49% Conservative: 61
Best Local Similarity: 32.23% Mismatches: 143
Query Match: 28.09% Indels: 0
LB: 3 Gaps: 0

US-09-898-586-24 (1-310) x US-08-748-506-9 (1-984)
CY 4 AsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIleGln 23
LB 31 AATGGGACTTTGGTCTCGAGTTCATCTCCTTGAGGGGTACCCGTGGCCGAGACACCTGAAG 90
CY 24 MetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGlyAsnGlyThr 43
LB 91 ATCCTCTTCTTCCCTACTGCACCTTGCTGGCCCTACTTGCCCTCATGGCCCAACATGCTC 150
CY 44 IleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhePheLeuSer 63
LB 151 ATAATTACCATCACCCTGCTGACCCAGCAGACGACCATGATGATCTTCTTCAGC 210
CY 64 HisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeuValAsn 83
LB 211 ACCTTCTCTTTGTGGAGCTGTGTTTATTAATACTACTGCTATCCCCACAGCTCTCACCATC 270
CY 84 LeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThrPheLeuPhe 103
LB 271 AATCTGTACAGGAGGCAAAAGATTCCCTTTGGCGTCTCTTCACAGGCCCTTCGCTAT 330
CY 104 SerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAspLeuTyrVal 123
LB 331 CTGTGCTGGGGGCAACAGTTTTCCTTTTGGCGTGTATCCCTGACCCCTTCTCTG 390
CY 124 AlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCysIleThrLeu 143
LB 391 GCCATCTGCAAAACCTCTACATTAATCCAAACATCATGAGCCCAAGAGTGTGCTCTCTC 450
CY 144 AlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 163
LB 451 GTTACTGCTGTTATTTTGGGCTTCCCTTCATGAGCCAGTCCAGTTGTGATGCTTCC 510
CY 164 ProLeuProPheCysArgProGlnIleTyrHisPhePheCysGluIleLeuAlaVal 183
LB 511 AAGACATTTTACTGTGTCCAAACATTAATTCCTCACTTTTCTGTGATTTGGACCACTG 570
CY 184 LeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAlaGlyAlaIle 203
LB 571 GCMAATCTCTCTCTTCAAGAAAGGCTCTATTTGAGATGCTGTTTTCACCTTGTGTA 630
CY 204 SerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIleLeuCysAla 223
LB 631 ATGTCCTTTTGTCTTCTTCTTAATAGCCATCTTTCATACGACAAATATAGTAGTACCC 690
CY 224 IleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSerHis 243
LB 691 ATAGTAGACTTCCCTTCAGCCAGGACGACAGAGAGCTTTTCCACCTGTCTCTCAT 750
CY 244 LeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyr 263
LB 751 CTCATTGTCTCTCTAATGATGACGACGTGCTGATTTATATACCTGAAGCCAAAGCAG 810
```

QY 264 GlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPheAsnPromet 283
DB 811 AGAAGCAGAGTGTGACACCAACAGAGAGCGCTGCTTGTGAACATGCTGTGACACCCCTT 870
QY 284 LeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgVal 303
DB 871 CTGAACCCCTGTCACTACACCCCTGCGCAACAAGCAGGTCCACCAAGCCTCTCAGGAGTCT 930
QY 304 Leu 304
DB 931 CTG 933

RESULT 13

US-09-668-680-13
; Sequence 13, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl-genes Version 2.0
; SEQ ID NO 13
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (130)..(1539)
US-09-668-680-13

Alignment Scores:

Seq. No.: 8.59e-39 Length: 1539
Score: 418.50 Matches: 96
Percent Similarity: 55.00% Conservative: 58
Best Local Similarity: 34.29% Mismatches: 119
Query Match: 26.01% Indels: 7
DB: 4 Gaps: 3

US-09-898-586-24 (1-310) x US-09-668-680-13 (1-1539)

QY 30 PheSerLeuPheTyrValPheThrLeuLeuGlyAsnGlyThrIleLeuGlyLeuIleSer 49
DB 682 TTCTGTGCCATGTATCTTGTAGCACCTGTGGTGAATGCTGCCCTCATCTGTCATTCGC 741
QY 50 LeuAspSerArgLeuHisAlaPrometTyrPhePheLeuSerHisLeuAlaValAlaSp 69
DB 742 ATGACCAATGCTCTTCATGACCACTATGTACCTCTTCTCTGCTTCTCTCACTCACAGAC 801
QY 70 IleAlaTyrAlaCysAsnThrValProArgMetLeuValAsnLeuLeuHisProAlaLys 89
DB 802 CTGGCTCTCAGTCTTACCACTGTGCCCAAGATGCTGGCCATTGTTGGCTCCATGCTGCT 861
QY 90 ProIleSerPheAlaGlyArgMetMetGlnThrPheLeuPheSerThrPheAlaValThr 109
DB 862 GAGATTCTCTTGTGGTGAATGCTGCCCAAGATGTTTGTGTCCATTCTATCTATGCTCTG 921

QY 110 GluCysLeuLeuLeuValAlaMetSerTyrAspLeuTyrValAlaIleCysHisProLeu 129
DB 922 GAGTCTCTGATTTCTACTTGGCATGCGCTTGTAGTATGTGGCTATCTGTAAACCATTA 981
QY 130 ArgTyrLeuAlaIleMetThrTrpArgValCysIleThrLeuAlaValThrSerTrpThr 149
DB 982 AGGTATACAAACCATTTCTCAACCATGCTGTGCATAGGCAAGAAATGGCTTTGTTGGCTATTC 1041
QY 150 ThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeuProLeuProPheCysArg 169
DB 1042 CGTAGTGTGGCTATGTCTCCCTTCCCTTCACTCTTCTTGTGAGGCGACTCCCTACTGTGCT 1101
QY 170 ProGlnLysIleTyrHisPhePheCysGluIleLeuAlaValLeuLysLeuAlaCysAla 189
DB 1102 CACCGTGTCAATGACACACACATACCTGTGAGCATATGGGCATGCGCCGACTGGCTGTGCC 1161
QY 190 AspThrHisIleAsnGluAsnMetValLeuAlaGlyAlaIleSerGlyLeuValGlyPro 209
DB 1162 -----AACATCACTGTCAATATGTCTATGGGCTAACTGTGGCTCTGCTGGCCATGGA 1215
QY 210 LeuSerThrIleVal-----ValSerTyrMetCysIleLeuCysAlaIleLeuGlnIle 227
DB 1216 CTGGATTCCATTTCTCATTTGCCATTTCTCTATGGCTTTATCTCCATGAGAGTCTTTCACCTT 1275
QY 228 GlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSerHisLeuCysValIle 247
DB 1276 CCATCTCATGATGCCACAGCAAAAGCTGTAGTACCTGTGGCTCCACATTTGGCATCATC 1335
QY 248 GlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyrGlyAsn----- 265
DB 1336 CTGGTTTCTACATCCCTGCCCTTCTCTCTCTTCCCTCAACCACCGCTTGGTCAACAGCAA 1395
QY 266 --ProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPheAsnPrometLeu 284
DB 1396 GTCCCCAAGCATGTGCACATCTTCTGTGGCTAATCTCTATGTGCTGGTGGCTCCTGTACTTC 1455
QY 285 AsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgValLeu 304
DB 1456 AATCCTATTCTCTATGTGAGCTAGAACCAAGAGATTGGAGTGCAGCTTCTAAACTGCTT 1515

RESULT 14

US-09-605-785-526
; Sequence 526, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 526
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-605-785-526

Alignment Scores:

Pred. No.:	4,12e-35	Length:	963
Score:	384.00	Matches:	100
Percent Similarity:	49.38%	Conservative:	58
Best Local Similarity:	31.25%	Mismatches:	126
Query Match:	23.87%	Indels:	36
DB:	4	Gaps:	8

US-09-898-586-24 (1-310) x US-09-605-785-526 (1-963)

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QY 4 AsnIleThrSerIleThrGluPheLeuLeuGlyPhePro----- 17
   ||| ||| ||| |||:||||:|||| |||
Db 13 AACTTCACACATGCCACC--TTTGTGCTTATTGGTATCCAGGATTAGAGAAAGCCCAT 69
QY 18 -----ValGlyProArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrVal 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 TTCTGGGTTGGC-----TTCCCTCTCTTCCATG--TATGTA 105
QY 36 PheThrLeuLeuGlyAsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHis 55
   ::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 GTGGCAATGTTTGGAAACTGCATCGTGTCTTCATCGTAGAGACGACGACGCTGCAC 165
QY 56 AlaProMetTyrPhePheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsn 75
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 GCTCCGATGTACCTTTCTCTGTCATGCTTGACACCATTCGCTTATCCACATCC 225
QY 76 ThrValProArgMetLeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGly 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 ACCATGCCCTAAGATCTTGCCCTTTTGTGTTGATTCCGAGAGATTAGCTTTGAGGCC 285
QY 96 ArgMetMetGlnThrPheLeuPheSerThrPheAlaValThrGlyCysLeuLeuVal 115
   ::| ||| ||| ||| |||:||||:|||| |||
Db 286 TGTCTTACCAGATGTTCTTATTATCATGCCCCCTCAGCCATTGAATCCACCATCTGCTG 345
QY 116 ValMetSerTyrAspLeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMet 135
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 GCCATGGCCTTGTGACCGTTATGTGGCCATTCGCCACCCACATGCGCATGTGCTGCTC 405
QY 136 ThrTrpArgValCysIleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSer 155
   ||| ||| ||| ||| |||:||||:|||| ||| ||| |||
Db 406 AACAAATACAGTAACAGCCACAGATGGCATCGTGCTGTCGCGGATCCCTCTTTT 465
QY 156 IleuIleHisLeuValLeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHis 175
   ::|||:||||:|||| ||| ||||| ||||| ||||| ||||| |||||
Db 466 TTCCCACTGCTGTGTGATCAAGCGGTGGCTTCTGCACTCCAAATGTCTCTCGCAC 525
QY 176 PhePheCysGluIleLeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGlu 195
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 526 TCCTATTGTGTCCACCAAGATGTAATGAAGTTGGCCTATGCAACACT----- 573
QY 196 AsnMetValLeuAlaGlyAlaIleSerGlyLeuValGlyProLeuSerThr----- 212
   ||| ||| ||| ||| |||:||||:|||| |||
Db 574 -----TTGCCCAATGCGTATATGCTTACTGCCATTCCTGCTGTCATGGCGCTG 624
QY 213 -----IleValIleSerTyrMetCysIleLeuCysAlaIleLeuGlnIleGln 228
   ||| ||| ||| ||| |||:||||:|||| |||
Db 625 GACGTAATGTTCAATCTCTTCTGCTATTTCTGATATACGACGCTTCTGCACTGCCCT 684
QY 229 SerArgGluValGlnArgLysAlaPheCysThrCysPheSerHisLeuCysValIleGly 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 TCCAACTCAGAGCGGCGCAAGCCCTTGGAACTGTGTACACATTTGGTGTGCTACCTC 744
QY 249 LeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyrGlyAsnProLysGlu 268
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 GCCCTCTATGTGCCACTTATTGGCCTCTCAGTTGTACACCGCTTTGGAACAGCCTTCAT 804
QY 269 GlnLysLysTyrLeuLeu-----PheHisSerLeuPheAsnProMetLeuAsnPro 286
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 CCCATGTGCGTGTGTGATGGGTGACATCTACCTGCTGCGCTCTGTCATCATATCCC 864
QY 287 LeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgValLeuGlyVal 306
```

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Db 865 ATCATCTATGTGTGCCAAACCAACACAGATCAGACACA-----CGGGTGTGCTATG 915
   ::||| ||| |||:||||:|||| |||
```

RESULT 15

US-09-439-313-526

Sequence 526, Application US/09439313

Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang Yugu

APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

FILE REFERENCE: 210121.427C9

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 526

LENGTH: 963

TYPE: DNA

ORGANISM: Homo sapiens

US-09-439-313-526

Alignment Scores:

Pred. No.:	4,12e-35	Length:	963
Score:	384.00	Matches:	100
Percent Similarity:	49.38%	Conservative:	58
Best Local Similarity:	31.25%	Mismatches:	126
Query Match:	23.87%	Indels:	36
DB:	4	Gaps:	8

US-09-898-586-24 (1-310) x US-09-439-313-526 (1-963)

```
QY 4 AsnIleThrSerIleThrGluPheLeuLeuGlyPhePro----- 17
   ||| ||| ||| |||:||||:|||| |||
Db 13 AACTTCACACATGCCACC--TTTGTGCTTATTGGTATCCAGGATTAGAGAAAGCCCAT 69
QY 18 -----ValGlyProArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrVal 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 TTCTGGGTTGGC-----TTCCCTCTCTTCCATG--TATGTA 105
QY 36 PheThrLeuLeuGlyAsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHis 55
   ::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 GTGGCAATGTTTGGAAACTGCATCGTGTCTTCATCGTAAGACGGAACGACGCTGCAC 165
QY 56 AlaProMetTyrPhePheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsn 75
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 GCTCCGATGTACCTTTCTCTGTCATGCTTGACACCATTCGCTTATCCACATCC 225
QY 76 ThrValProArgMetLeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGly 95
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Db 226 ACCATGCCCTAAGATCTTGCCCTTTTGTGTTGATTCCGAGAGATTAGCTTTGAGGCC 285
QY 96 ArgMetMetGlnThrPheLeuPheSerThrPheAlaValThrGlyCysLeuLeuVal 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 TGTCTTACCAGATGTTCTTATTATCATGCCCCCTCAGCCATTGAATCCACCATCTGCTG 345
QY 116 ValMetSerTyrAspLeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMet 135
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Db 346 GCCATGGCCTTGTGACCGTTATGTGGCCATCTGCCACCCACTGCGCCATGCTGCACTGCTC 405
QY 136 ThrTrpArgValCysIleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSer 155
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Db 406 AACAAATACAGTAACAGCCACAGATGGCATCGTGTGCTGCTGCGGATCCCTCTTTT 465
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 2, 2003, 08:42:37 ; Search time 805 Seconds
(without alignments)
166.554 Million cell updates/sec

Title: US-09-898-586-24
Perfect score: 1609
Sequence: 1 MGDNITSITEFLLGFPVGP.....LRNSEVKNTLKRVLGERAL 310

Scoring table: BIOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1609	100.0	1012	10	US-09-761-288-21 Sequence 21, Appl
2	1584	98.4	1040	10	US-09-761-288-3 Sequence 3, Appl
3	1584	98.4	1040	10	US-09-761-288-34 Sequence 34, Appl
4	1568	97.5	1014	10	US-09-761-288-23 Sequence 23, Appl

5	1147	71.3	2282	9	US-10-098-841-92	Sequence 92, Appl
6	1147	71.3	2282	10	US-09-747-835A-62	Sequence 62, Appl
7	1138	70.7	1788	10	US-09-747-835A-35	Sequence 35, Appl
8	1138	70.7	2735	10	US-09-747-835A-34	Sequence 34, Appl
9	1126	70.0	933	10	US-09-864-761-30527	Sequence 30527, A
10	1126	70.0	1957	10	US-09-864-761-13963	Sequence 13963, A
11	1080	67.1	927	10	US-09-747-835A-43	Sequence 43, Appl
12	1080	67.1	1782	10	US-09-747-835A-41	Sequence 41, Appl
13	991	61.6	933	10	US-09-886-055-484	Sequence 484, App
14	947.5	58.9	930	10	US-09-886-055-472	Sequence 472, App
15	930	57.8	933	10	US-09-886-055-486	Sequence 486, App
16	881	54.8	936	10	US-09-886-055-482	Sequence 482, App
17	790	49.1	456	10	US-09-812-102-72	Sequence 72, Appl
18	692	43.0	939	10	US-09-886-055-440	Sequence 440, App
19	670.5	41.7	936	10	US-09-886-055-10	Sequence 10, Appl
20	670	41.6	1008	10	US-09-886-055-452	Sequence 452, App
21	669	41.6	942	10	US-09-771-209-3	Sequence 3, Appl
22	669	41.6	957	10	US-09-886-055-226	Sequence 226, App
23	668	41.5	939	10	US-09-886-055-26	Sequence 26, Appl
24	666	41.4	939	9	US-10-032-106-2	Sequence 2, Appl
25	666	41.4	942	10	US-09-755-017-1	Sequence 1, Appl
26	666	41.4	1488	10	US-09-755-017-3	Sequence 3, Appl
27	661.5	41.1	995	10	US-09-771-730-31	Sequence 31, Appl
28	661	41.1	1053	10	US-09-886-055-398	Sequence 398, App
29	660.5	41.1	930	10	US-09-771-730-110	Sequence 110, App
30	660.5	41.1	993	10	US-09-886-055-200	Sequence 200, App
31	660.5	41.1	994	10	US-09-771-730-23	Sequence 23, Appl
32	660	41.0	951	10	US-09-886-055-180	Sequence 180, App
33	659.5	41.0	921	10	US-09-771-730-135	Sequence 135, App
34	659.5	41.0	960	10	US-09-771-730-21	Sequence 21, Appl
35	659.5	41.0	968	10	US-09-771-730-35	Sequence 35, Appl
36	659.5	41.0	994	10	US-09-771-730-139	Sequence 139, App
37	658.5	40.9	921	10	US-09-771-730-134	Sequence 134, App
38	658.5	40.9	994	10	US-09-771-730-25	Sequence 25, Appl
39	658.5	40.9	994	10	US-09-771-730-33	Sequence 33, Appl
40	658.5	40.9	994	10	US-09-771-730-138	Sequence 138, Appl
41	656	40.8	975	10	US-09-886-055-326	Sequence 326, App
42	656	40.8	1954	10	US-09-864-761-5098	Sequence 5098, App
43	655.5	40.7	930	10	US-09-771-730-111	Sequence 111, App
44	653	40.6	975	10	US-09-886-055-498	Sequence 498, App
45	653	40.6	1023	10	US-09-886-055-466	Sequence 466, App

ALIGNMENTS

RESULT 1
US-09-761-288-21
Sequence 21, Application US/09761288
Patent No. US20020065405A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tehernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26

; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-21

Alignment Scores:
Pred. No.: 2,76e-163 Length: 1012
Score: 1609.00 Matches: 310
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-761-288-21 (1-1012)

1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuLeuGlyPheProValGlyPro 20
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21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
|||||
114 AGGATTTCAGATGCTCTCTTGGGCTCTCTCCCTGTTCTACGCTTCACCCCTGTGGGG 173
41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
|||||
174 AACGGACCATACTGGGGCTCATCTCAGACTGCACGCCCCCATGTACTTC 233
61 PheLeuSerHisLeuAlaValValAspIleAlaTyrAlaCysAsnThrValProArgMet 80
|||||
234 TTCCTCTACACCTGGGGCTGTCGACATGCGCTTACGCTCAACACGGGTGCCCCGGATG 293
81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
|||||
294 CTGGTGAACCTCCGTCATCCAGCAAGCCCATCTCTTGGGGCCGCATGATGCAGACC 353
101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
|||||
354 TTCTGTGTTTCCACTTTTGGCTGTACAGAAATGTCTCTCTGCTGGTGATGTCTATGAT 413
121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
|||||
414 CTGTACGTGGCCATGTGCCACCCCTCGCATATTGGCCATCATGACCTGGAGAGTGTGC 473
141 IleThrLeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuVal 160
|||||
474 ATCACCCTCGGGGTGACTTCTCGGACCATGGAGTCTTTATCTTATCTTCAATCTTGTG 533
161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
|||||
534 TTACTTCTTACCTTACCTTCTGTAGGCCCCAGAAAATTATATCACTTTTGTGAAATC 593
181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
|||||
594 TTGGCTGTCTCAAACTTGCCCTGTGCAGATACCCACATCAATGACAACATGTGCTTGGCC 653
201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
|||||
654 GGAGCAATTTCTGGGCTGTGGGACCCCTGTGCCACAAATTTAGATTTCATATATGTGCATC 713
221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
|||||
714 CTCTGTGCTATCTTCAGATCCAAATCAAGGGAAGTTCAAGAGAAAGCCTTCTGCACCTGC 773
241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
|||||
774 TTCTCCACACCTGTGTGATGTGACTCTTTTATGCGACAGCCCATATCATGATGTGGA 833

261 ProArgTyrGlyAsnProLysGlnGlnLysTyrLeuLeuPheHisSerLeuPhe 280
|||||
834 CCCAGATATCGGAACCCCAAGAGCAGAGAAATATCTCTGCTGTTCACAGCCTCTTT 893
281 AsnPrometLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
|||||
894 AATCCATGCTCAATCCCTTATCTGTAGTCTTACGAACCTCAGAAGTGAAGAAATACTTTG 953
301 LysArgValLeuGlyValGlnArgAlaLeu 310
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954 AAGAGAGTCTGGGAGTAGAAGGCTTTTA 983

RESULT 2

US-09-761-288-3
; Sequence 3, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1e1 Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-3

Alignment Scores:

Pred. No.: 1,36e-160 Length: 1040
Score: 1584.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 3
Query Match: 98.45% Indels: 0
DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-761-288-3 (1-1040)

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21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
|||||
142 AGGATTTCAGATGCTCTCTTGGGCTCTTCTCCCTGTTCACGCTTTCACCTGTGGGG 201
41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
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Db 262 TTCTCTCACACCTGGCGGTCGTGACATCGCCTACGCTGCACACACGCGCCCGGATG 321
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 322 CTGGTGAACCTCCTGCATCCAGCAAGCCCATCTCTTGGCGGCCCATGATGACAGACC 381
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
Db 382 TTTCTGTTCACACTTTTGGCTGTACAGAAATGTCTCTCCCTGGTGGTGAATGAT 441
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 442 CTGTACGTGGCCATCTGCACACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGC 501
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Db 502 ATCACCCCTCGCGGTGACTTCCTGGACCACTGAGATCCTTTATCTTGATTCATCTTGTG 561
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 562 TTACTTCTACCTTTACCTCTGTGTAGGCCCCAGAAATTATCATTCTTTTGTGAATC 621
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Db 802 TTCTCCCACTCTGTGTGATGGACTCGTTATGGCACAGCCATTATCATGATGTTGGA 861
QY 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 862 CCCAGATATGGGAACCCCAAGAGCAGAGAATAATATCTCTGCTGTTTCACAGCCTCTT 921
QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
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Db 982 AAGAGAGTGTGGAGTAGAAGGCTTTA 1011

RESULT 3
US-09-761-288-34
; Sequence 34, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
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; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-34

Alignment Scores:
pred. No.: 1,36e-160 length: 1040
Score: 1584.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best Local Similarity: 99.03% Mismatches: 3
Query Match: 98.45% Indels: 0
DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-761-288-34 (1-1040)
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QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 142 AGCATTCAGATGCTCTCTTTGGGCTCTCTCCCTGTTCTACGCTTCAACCTGCTGGGG 201
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
Db 202 AACGGACCATACTGGGCTCATCTCACTGGACTCCAGACTGCACGCCCATGTACTTC 261
QY 61 PheLeuSerHisLeuAlaValAlaSpIleAlaIleTyrAlaCysAsnThrValProArgMet 80
Db 262 TTCTCTCACACCTGGCGGTCGTGCACATCGCCTACGCTGCACACGCGCCCGGATG 321
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 322 CTGGTGAACCTCCTGCATCCAGCAAGCCCATCTCTTGGCGGCCCATGATGACAGACC 381
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
Db 382 TTTCTGTTCACACTTTTGGCTGTACAGAAATGTCTCTCTGCTGGTGTGATGCTATGAT 441
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 442 CTGTACGTGGCCATCTGCACACCCCTCCGATATTGGCCATCATGACCTGGAGAGTCTGC 501
QY 141 IleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 502 ATCACCCCTCGCGGTGACTTCCTGGACCACTGAGATGCTCTTATCTTGATTCATCTGTG 561
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 562 TTACTTCTACCTTTACCTTCTGTAGGCCCCAGAAATTATCATTCTTTTGTGAATC 621
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 622 TTGGCTGTCTCAAACTGCTGCTGACAGATACCCACATCAATGAGAACATGCTTGGCC 681
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
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Db 682 GGAGCAATTTCGGCTGGTGGCACCCTTGTCACAATTGTAGTTTCATATATATGTCATC 741
QY 221 LeuCySAIaIleIeuGlnIleGlnSerArgIuValGlnArgIysAlaPheCysThrCys 240
Db 742 CTTGTGCTATCTTCAGATCCAAATCAAGGAGTTCAAGAAAGCCCTTCGACACCTGC 801
QY 241 PheSerHisLeuCySAIleGlyLeuPheTyGlyThrAlaIleIleMetTyValGly 260
Db 802 TTCTCCACCTCTGTGTGATGTGACCTGTTATGACACAGCCATTCATGTATGTTGGA 861
QY 261 ProArgTyGlyAsnProIysGluGlnIlySlyTyrrLeuLeuPheHisSerLeuPhe 280
Db 862 CCCAGATATGGGAACCCCAAGAGCAGAGAATAATCTCCTGCTTTCACAGCCCTTT 921
QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValIlyAsnThrLeu 300
Db 922 AATCCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACCTCAGAAAGTGAATACTATTG 981
QY 301 LysArgValIleuGlyValGluArgAlaLeu 310
Db 982 AAGAGAGTCTGCGAGTAGAAGGCGCTTTA 1011

RESULT 4

US-09-761-288-23
; Sequence 23, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-23

Alignment Scores:
Pred. No.: 6.79e-159 length: 1014
Score: 1568.00 Matches: 309
Percent Similarity: 99.36% Conservative: 0
Best Local Similarity: 99.36% Mismatches: 1
Query Match: 97.45% Indels: 2
DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-761-288-23 (1-1014)

QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20

Lb 55 ATGGGGCACAATATATACATCCATCAGAGACTTCCTCTACTGGGATTTCCCGTTGGCCCA 114
Cy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrrValPheThrLeuGly 40
Lb 115 AGGATTCAGATGCTCTCTTTGGGCTTCTCCCTGTTCAGTCTTACCCCTGCTGGGG 174
Cy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrrPhe 60
Lb 175 AACGGGACCATACTGGGGCTCATCTCAGTGGACTCCAGACTGCACGCCCTG-TACTTC 233
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrrAlaCysAsnThrValProArgmet 80
Lb 234 TTCTCTCACACCTGGCGGCTGTCGACATCGCCTAGCGCTGCACACCGGTGCCCGGATG 293
QY 81 LeuValAsnLeuLeuHisProAlaIlyProIleSerPheAlaGlyArgMetGlnThr 100
Lb 294 CTGGTGAACCTCTGTCATCCAGCCAGCCCATCTCCTTGGGGGCCGATGATGACAGACC 353
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrrAsp 120
Lb 354 TTCTGTGTTTCCACTTTTGTCTGTCCACAGATGTCCTCTCTGTGTGTGATGCTCATGAT 413
QY 121 LeuTyrrValAlaIleCysHisProLeuArgTyrrLeuAlaIleMetThrTrpArgValCys 140
Lb 414 CTGTAGCTGGCCATCTGCCACCCCTCCGATATTTGGCCATCATGACCTGGAGAGTCTGC 473
QY 141 IleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Lb 474 ATCACCCCTCGCGGTGACTTCTCTGAGCACCACTGGAGCTCTTATCTTGAATTCATCTTGTG 533
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnIlySlyIleTyrrHis-PhePheCysGluIle 180
Lb 534 TTACTTCTACCTTACCTTCTGTAGAGCCCAAGAAATTTATCATTCTTTTGTGAAAT 593
QY 180 eLeuAlaValLeuIlyLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAl 200
Lb 594 CTTGGCTGTTCTCAACTTGGCTGTGAGATACCCACATCAATGAGAACATGGTCTTGGC 653
QY 200 aGlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValIleSerTyrrMetCysIle 220
Lb 654 CCGAGCAATTTCGGGCTGTGGGACCCTTGTCCACAATTGTAGTTTCATATATGTGCAT 713
QY 220 eLeuCySAIaIleIeuGlnIleGlnSerArgIuValGlnArgIysAlaPheCysThrCy 240
Lb 714 CTTCTGTCTATCTTCAGATCCAAATCAAGGAGAGTTCAAGAGAAAGCCCTTCACACCTG 773
QY 240 sPheSerHisLeuCySAIleGlyLeuPheTyrrGlyThrAlaIleIleMetTyrrValGly 260
Lb 774 CTTCTCCACCTCTGTGTGATTTGGACTCTTTATGGCACAGCATTCATGTATGTTGG 833
QY 260 yProArgTyrrGlyAsnProIysGluGlnIlySlyTyrrLeuLeuPheHisSerLeuPhe 280
Lb 834 ACCAGATATGGGAACCCCAAGAGCAGAGAATAATATCTCTGCTGTTCCACAGCCCTCTT 893
QY 280 eAsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValIlyAsnThrLe 300
Lb 894 TAAATCCATGCTCAATCCCTTATCTGTAGTCTTAGGAACTCAGAAGTGAAGATACTATT 953
QY 300 uLysArgValIleuGlyValGluArgAlaLeu 310
Lb 954 GAAGAGAGTCTGCGAGTAGAAGGCGCTTTA 984

RESULT 5

US-10-098-841-92
; Sequence 92, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping

APPLICANT: Ma, Yunging
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PL_FL_genes Version 1.0
SEQ ID NO 92
LENGTH: 2282
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1257)..(2189)
US-10-098-841-92

Alignment Scores:
Pred. No.: 2.61e-113 Length: 2282
Score: 1147.00 Matches: 220
Percent Similarity: 84.87% Conservative: 38
Best local Similarity: 72.37% Mismatches: 46
Query Match: 71.29% Indels: 0
DB: 9 Gaps: 0

US-09-898-586-24 (1-310) x US-10-098-841-92 (1-2282)

QY 1 MetGlyAspAsnIleThrserIleThrgluPheLeuLeuGlyPheProValGlyPro 20
DB 1257 ATGGTGAATAATCAGACAAATGTCACAGAGTTCTCTACTGGATTCTCTGGCCCA 1316
21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
DB 1317 AGGATTGAGATGCTCCTCTTGGGCTCTTCTCTCTGTTCTATGCTTCACCCCTGCTGGG 1376
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
DB 1377 AATGGACCATCTCTGGGGCTCATCTCACTGGACTCCAGACTCCACACCCCATGTACTTC 1436
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
DB 1437 TTCTCTCACACCTGGCGCTGCTCAACATGCGCTATGCTGCACACAGTGCCTCAGATG 1496
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
DB 1497 CTGGTGAACCTCTCTGCATCCAGCCCAAGCCCATCTCTTGGCTGGCTGCATGACACAGACC 1556
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValAlaMetSerTyrAsp 120
DB 1557 TTCTCTTTTGTGAGTTTGCACATACATGAATGCTCTCTGTTGGTGCATGTCTCAGAT 1616
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
DB 1617 CGGTACGTGGCCATCTGCACACCTCTCCGATATTTCATCATCATGACCTGGAAAGTCTGC 1676
QY 141 IleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160

DB 1677 ATCACTTGCGCCATCACTTCTCTGGACATGTGGCTCCTCTGCTATGATGCTCATGTGACC 1736
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
DB 1737 CTCACTCTAAGACTGCCCCCTTTGTGGCCCTGCTGTAATCAACCACTTCTCTGTGAATC 1796
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
DB 1797 CTGTCTGCTTCAGGCTGGCGCTGTGCTGATACCTGCTCAACCAAGGTGCATCTTTGCA 1856
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
DB 1857 GCCTGCATGTTTCATCTCTGGTGGACCACTCTGCTGTGCTGTGCTCTACTACACATC 1916
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
DB 1917 CTGGCGGCGCATCTCGAGGATCCAGTCTGGGGAGGGCGCCAGAAAGGCTTCTCCACCTGC 1976
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
DB 1977 TCCTCCCACTCTGCGTAGTGGAACCTCTTCTTTGGCAGCCGCATCTCATGTACATGGCC 2036
QY 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
DB 2037 CCTAAGTCCCGCCATCTCTGAGGACAGCAGAAAGGCTCTTTTCTATTATTACAGTCTTTC 2096
QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
DB 2097 AACCGATGTCTAAACCCCTGATTTCACACCTGAGGATGTAGAGGTCAAGGGTGCCTG 2156
QY 301 LysArgValLeu 304
DB 2157 AGGAGAGCACTG 2168
RESULT 6
US-09-747-835A-62
Sequence 62, Application US/09747835A
Patent No. US20020146692A1
GENERAL INFORMATION:
APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Wang, Dunrui
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L
TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HXS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 62
LENGTH: 2282
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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Db 725 CTGGTGAACCTCCTGCATCCAGCCAGCCCATCTCTTGCTGGCTGCATGACATAGACC 784
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 785 TTTCTCTTTTGGATTGGACATACTGAATGCTCTGTTGGTGGATGTCCTACGAT 844
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 845 CGGTACGTGGCCATCTGCCACCTCTCCGATATTTCATCATCATGACCTGGAAGCTGC 904
Qy 141 IleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 905 ATCACTCTGGCCATCACTTCCTGGACATGTGGCTCCCTGGCTATGATGTCATGTGAGC 964
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 965 CTCACTCCTAAGACTGCCCTTTGTGGCCCTCGTGAATCAACCACTTCTCTGTGAATC 1024
Qy 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 1025 CTGTCTGTCTCAGCTGGCTGTGCTGATACCTGCTCAACCAAGGTGCATCTTTGCA 1084
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 1085 GCCTGCATGTTTCATCCTGTGGGACCACTCTGCTGGTGTGCTCTCTACTCACACATC 1144
Qy 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 1145 CTGGCGCCATCCTGAGGATCCACTCTGGGAGGGCCGACAGAAAGCCCTTCTCCACCTGC 1204
Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 1205 TCCCTCCACCTCTGCGTAGTGGACTCTTCTTTGGCAGCGCCATCGTCAATGATGACC 1264
Qy 261 ProArgTyrGlyAsnProLysGluGlnLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 1265 CCTAAGTCCCGCCATCCTGAGGAGCAGAGAGAGTCCCTTTTCTATTTCAGTCTTTC 1324
Qy 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
Db 1325 AACCCGATGCTAAACCCCTGATTTACAACCTGAGGAATGTAGAGGTCAAGGGTGCCCTG 1384
Qy 301 LysArgValLeu 304
Db 1385 AGGAGAGCACTG 1396
SUBT 8
US-09-747-835A-34
; Sequence 34, Application US/09747835A
; Patent No. US20020146692A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
; TITLE OF INVENTION: (LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747, 835A
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/729, 739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598, 042

; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 2735
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-835A-34
Alignment scores:
Pred. No.: 3,12e-112 Length: 2735
Score: 1138.00 Matches: 219
Percent Similarity: 84.54% Conservative: 38
Best Local Similarity: 72.04% Mismatches: 47
Query Match: 70.73% Indels: 0
DB: 10 Gaps: 0
US-09-898-586-24 (1-310) x US-09-747-835A-34 (1-2735)
Qy 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1335 ATGGTGAATAATCAGACAAATGTCACAGAGTTCCTCTACTGGGATTTCTCTGGGCCA 1394
Qy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 1395 AGGATTCAGATGCTCTCTTTGGGCTCTCTCCCTGTCTATGCTTCAACCTGCTGGGG 1454
Qy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
Db 1455 AATGGACCATCCTGGGCTCATCTCACAGGACTCCAGACTGCACACCCCATGTACTTC 1514
Qy 61 PheLeuSerHisLeuAlaValValAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 1515 TTCTCTCACACCTGCGCGTCTGTCACAACTCGCTATGCTGCAACACAGTGGCCCATG 1574
Qy 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 1575 CTGGTGAACCTCCTGCATCCAGCCAGCCCATCTCTTGTGGCTGCATGACATAGACC 1634
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
Db 1635 TTTCTCTTTTGGATTTTGGACACATAGTAATGCTCTGTTGGTGTGATGTCCTACGAT 1694
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 1695 CGGTACGTGGCCATCTGCCACCTCTCCGATATTTCATCATCATGACCTGGAAGTCTGC 1754
Qy 141 IleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 1755 ATCACTCTGGCCATCACTTCCTGACATATGGCTCCCTGCTATGTCATGTGAGACC 1814
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 1815 CTCACTCCTAAGACTGCCCTTTGTGGCCCTCGTGAATCAACCACTTCTCTGTGAATC 1874
Qy 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 1875 CTGTCTGTCTCAGGTGGCTGTGCTGATACCTGCTCAACCAAGGTGTGATCTTGCA 1934
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 1935 GCCTGCATGTTTCATCCTGTGGGACCACTCTGCTGTGCTGCTCTACTCACACATC 1994
Qy 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 1995 CTGGCGCCATCCTGAGGATCCAGTCTGGGAGGGCCGACAGAAAGCCCTTCTCCACCTGC 2054
Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
|||||

Db 2055 TCCTCCACCTCTGCGTAGTGGGACTCTTCTTTGGCAGCGCCATCGTATGTACATGGCC 2114
QY 261 ProarglytyrGlyAsnProlysgluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 2115 CCTAAGTCCCGCCATCCTGAGAGACAGCAGAGAGGTCCTTTCTATTTTACAGTTCTTTC 2174
QY 281 AsnProMetLeuAsnProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 300
Db 2175 AACCCGATGCTAAACCCCGCTGATTACACCTGAGGAATGTAGAGTCAAGGCGCTG 2234

QY 301 LysArgValLeu 304
Db 2235 AGGAGAGCAGCTG 2246

RESULT 9

US-09-864-761-30527/c
; Sequence 30527, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30527

LENGTH: 933

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC004889.1
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P34984, EVALUATE 1.00e-86
; OTHER INFORMATION: EST_HUMAN HIT: BF116115.1, EVALUATE 0.00e+00
; OTHER INFORMATION: NT HIT: U86281.1, EVALUATE 0.00e+00
US-09-864-761-30527

Alignment Scores:

Pred. No.:	1.28e-111	Length:	933
Score:	1126.00	Matches:	219
Percent Similarity:	82.08%	Conservative:	33
Best Local Similarity:	71.34%	Mismatches:	55
Query Match:	69.98%	Indels:	0
DB:	10	Gaps:	0

US-09-898-586-24 (1-310) x US-09-864-761-30527 (1-933)

QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 930 ATGGGGGAAATCAGACAAATGCTCAGAGATTCTCTACTGGGATTTCTCCGGGCCCA 871
QY 21 ArgIleGlnMetLeuPheGlyLeuPheSerLeuPheThrValPheThrLeuGly 40
Db 870 AGGATTCAGATGCTCCTTTGGGCTCTTCCCTGTTCTATATCTTACCCCTGGGG 811
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
Db 810 AACGGGGCATCTGGGGCTCATCTCAGTGGACTCCAGACTCCACCCCATGTAAGTTC 751
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 750 TTCTCTCACACCTGGCTGCTGCTGACATGCGCTACACCCGCAACACGGTCCAGATG 691
QY 81 LeuValAsnLeuLeuHisProAlaIleProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 690 CTGGGGAACCTCTGCAATCCAGCCCAAGCCATCTCTTGGTGGTGCATGAGCAGACC 631
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValAlaMetSerTyrAsp 120
Db 630 TTCTCTGTTTGGAGTTTGGACACACAGCAATGCTCTCTGCTGCTGATGCTTACGAT 571
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
Db 570 CGTTACGTGGCCATCTGCCACCTCTCCGATACCTCCGTCATATGACCTGGAGATCTGC 511
QY 141 IleThrLeuAlaValThrSerThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 510 ATCACCTGGCCGCTGACTCTGAGACGATGGCTCCCTGCTGCTGCTGCTGCTGCTGCT 451
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 450 CTGATCCTAAGACTGCGCTTCTCTGCGCTCATGAAATCAACCACTTCTCTGGAATC 391
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 390 CTGCTGTCTCAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 331
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValAlaSerTyrMetCysIle 220
Db 330 GCGTGGCTGTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnAlaGlyAlaPheCysThrCys 240
Db 270 CTGGGGGCATCTCTGAGCATCCAGTCTGGGAGGGGCCGACAAAGCCCTTCTCCACCTGC 211
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 210 TCCTCCACCTGCTGGCTGGAGCTCTTCTTGGCAGTGGCCATCATGATGATGAGGCC 151
QY 261 ProArgTyrGlyAsnProlysgluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280


```
||||:|:||||:||||:||||:|
Db 150 CCCAAGTCCCGCCATCTCTGAGGAGCAGCAAAAGCTTTTCTATTTTACAGTTTTC 91
QY 281 AsnPrometleuAsnProleuileCysSerleuArgAsnSerGluVallyAsnThrleu 300
Db 90 AACCCACACTTAACCCCTGATTTACAGCCTGAGGAGACGAGAGGTCAAGGGTCCCTG 31
QY 301 LysArgValleuGlyValGlu 307
Db 30 AGGAGAGCACTGGGCAAGGAA 10
```

RESULT 10

US-09-864-761-13963/c

; Sequence 13963, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 13963

; LENGTH: 1957

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC004889.1

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
US-09-864-761-13963
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Alignment Scores:

Pred. No.:	3,72e-111	Length:	1957
Score:	1126.00	Matches:	219
Percent Similarity:	82.08%	Conservative:	33
Best Local Similarity:	71.34%	Mismatches:	55
Query Match:	69.98%	Indels:	0
DB:	10	Gaps:	0

US-09-898-586-24 (1-310) x US-09-864-761-13963 (1-1957)

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QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1054 ATGGGGGAAAATCAGACAAATGTCACAGAGTTCCCTCTACTGGGATTTCTGCGGCCCA 995
QY 21 ArgIleGluMetLeuLeuPheGlyLeuPheSerLeuPheThrValPheThrLeuGly 40
Db 994 AGGATTCAGATGCTCTCTTTGGGCTCTTCTCCCTGTCTATATCTTACACCTGCTGGGG 935
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
Db 934 AACGGGGCAATCTGGGGCTCATCTCAGACTCCAGACTCCACACCCCAATGTACTTC 875
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 874 TTCTCTCTACACCTGCTGCTGTGTCGACATCGCTTACACCGGCAACAGGTCGCCAGATG 815
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 814 CTGGCGAACCTCTGTCATCCAGCCAGCCCATCTCTGCTGCTGCTGATGACGACAGACC 755
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValAlaMetSerTyrAsp 120
Db 754 TTCTCTGTTGAGATTGTTGGACACACGGAATGTCCTCTGCTGCTGCTGATGTCCTACGAT 695
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrrArgValCys 140
Db 694 CGTTACGTGGCCATCTGCCACCCCTCTCCGATACTCCGTCATCATGACCTGGAGAGTCTGC 635
QY 141 IleThrLeuAlaValThrSerTrrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 634 ATCACCCCTGGCCCTGCTCCAGCTGTGGCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTG 575
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 574 CTCATCTTAAGACTGCCCTTCTCTGGGCTCATGAATCAACCACTTCTTCTGTGAATC 515
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 514 CTCTCTCTCTCAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 455
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValIleSerTyrMetCysIle 220
Db 454 GCCTGGCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 394 CTGGCGGCCATCTCGAGGATCCAGCTGTGGGAGGCGCCGCAAGGCCCTTCTCCACCTGC 335
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 334 TCCTCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275
QY 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 274 CCCAAGTCCCGCCATCTGAGAGCAGCAAAAGTCTTTTCTATTTTACAGTTTTC 215
QY 281 AsnPrometleuAsnProleuileCysSerleuArgAsnSerGluVallyAsnThrleu 300
Db 214 AACCCACACTTAACCCCTGATTTTACAGCCTGAGGAACGAGAGGTCAAGGGTCCCTG 155
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OY 301 lysArgValleuGlyValGlu 307
:::|||||
DB 154 AGGAGAGCAGCTGGGCAAGGAA 134

RESULT 11
US-09-747-835A-43
; Sequence 43, Application US/09747835A
; Patent No. US20020146692A1

; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Yang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747, 835A
; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: US 09/729, 739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-835A-43

Alignment Scores:
Pred. No.: 1.07e-106 Length: 927
Score: 1080.00 Matches: 211
Percent Similarity: 81.91% Conservative: 38
Best Local Similarity: 69.41% Mismatches: 53
Query Match: 67.12% Indels: 2
Gaps: 1

US-09-898-586-24 (1-310) x US-09-747-835A-43 (1-927)

OY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
||| ||| ::|||
DB 1 ATGGTGAATAATCAGACAAATGGTCACAGAGTTCCTCTACTGGGATTTCTCTGGGCCCA 60
OY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
|||||
DB 61 AGGATTCAGATGCTCTTGGGCTCTCTCCCTGTCTATATCTTCACCCCTGCTGGGG 120
OY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
|||||
DB 121 AACGGGGCCATCTGGGCTCATCTCAGCTGCACTCCATACCCCCATGTACTTC 180
OY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
|||||
DB 181 TTCCTCTCACACCTGGCTGTCTGACATCGCTTACACCCGCAACACGGTGCCTCAGATG 240
OY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
||| |||
DB 241 CTGGCGAACCTCTCTGATCCAGCCCAAGCCCATCTCTTGGCTGTGATGACGACGAGACC 300

OY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
|||||
DB 301 TTCTCTGTGTGAGTTTGGACACACAGCGAATGTCTCTGCTGGTGTGATGTCTTACGAT 360
OY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
|||||
DB 361 CGTTACGTGGCCATCTGCCACCCCTCTCCGATACCTCCGTCATCATGACC-----TGCATG 414
OY 141 IleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
|||||
DB 415 ATCACTCTGGCCATCACTTCTCGACATGTGGCTCCCTGCTGATGTGTCATGTGAGC 474
OY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
|||||
DB 475 CTCATCTTAAGACTGCCCTTTTGTGGGCTCGTGAATCAACCCACTTCTTCTGTGAATC 534
OY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
|||||
DB 535 CTGTCTGTCTCAGGCTGGCTGTGCTGATACCTGGCTCAACCAAGCTGTCATCTTTCGA 594
OY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
:::
DB 595 GCCTGCATGTTCATCTGTGTGGAGCACACTGTGCTGTGCTGTCTTCTACTCACACATC 654
OY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
||| |||
DB 655 CTGGCGGCATCTCTGAGATCAGTCTGGGAGGGCCGCAAGAGCCTTCTCCACCTGC 714
OY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
|||||
DB 715 TCCTCCACCTCTGCTGATGTGGACTCTTCTTGGCAGCGCCATCTCATGTACATGGCC 774
OY 261 ProArgTyrGlyAsnProLysGluGlnLysTyrLeuLeuLeuPheHisSerLeuPhe 280
||| :::
DB 775 CCTAAGTCCCGCCATCTCTGAGAGCAGCAGAGAGTCTTTCTATTTTACAGTTCCTTC 834
OY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
|||||
DB 835 AACCGATGCTAAACCCCTGATTTTACACCTGAGGAATGTAGAGTCAAGGTGCCCTG 894
OY 301 LysArgValIleu 304
:::|||||
DB 895 AGGAGAGCACTG 906

RESULT 12
US-09-747-835A-41

; Sequence 41, Application US/09747835A
; Patent No. US20020146692A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747, 835A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/729, 739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552, 317

: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 63
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 41
: LENGTH: 1782
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (485)..(1411)
US-09-747-835A-41

Alignment Scores:
Pred. No.: 2,74e-106 Length: 1782
Score: 1080.00 Matches: 211
Percent Similarity: 81.91% Conservative: 38
t Local Similarity: 69.41% Mismatches: 53
Query Match: 67.12% Indels: 2
DB: 10 Gaps: 1

US-09-898-586-24 (1-310) x US-09-747-835A-41 (1-1782)

QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
DB 485 ATGCTGAAAAATCAGACAAATGTCACAGAGTTCTCTCTACTGGATTCTCTGGGCCCA 544
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
DB 545 AGGATTCAGATGCTCTCTTTGGGGCTCTCTCCCTGTTCTATATCTTCACCCCTGCTGGG 604
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
DB 605 AACGGGGCCATCCTGGGGCTCATCTCAGCTGACTCCAGACTCCATACCCCATGACTTTC 664
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
DB 665 TTCTCTCTCAGACCTGGCTGTGTCGACATCGCTACACCCGCAACAGCGCCCAAGATG 724
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
DB 725 CTGGCGAACCTCTCCATCCAGCCCAAGCCCATCTCTTGCTGGTTCATGACGACAGACC 784
QY 101 PheLeuPheSerThrPheAlaValAlaThrGlyCysLeuLeuLeuValValMetSerTyrAsp 120
DB 785 TTCTCTGTGTTGAGTTTGGACACAGCAATGTCTCTGCTGGTGTGCTGATGCTTACGAT 844
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
DB 845 CGTTACGTGGCCATCTGCCACCCCTCCGATACTCCGTCATCATGACCC-----TGCTGC 898
QY 141 IleThrLeuAlaValIleThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
DB 899 ATCACTCTGGCCATCACTTCTCTGGACATGTGGCTCCCTCTGGCTATGCTCATGTGAGC 958
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
DB 959 CTCACTCTTAAGACTGCCCTTTTGTGGGCTCGTGAATCAACCACTTCTTCTGTGAATC 1018
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAla 200
DB 1019 CTGTCTGTCTCAAGCTGGGCTGTGCTGATACCTGGCTCAACCAAGGTGTCATCTTGA 1078
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
DB 1079 GCCTGCATGTTTCATCTCTGGTGGGACCACTCTGCCCTGTGCTGTCTCTCTACACATC 1138
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
DB 1139 CTGGCGGCATCTCTGAGCATCCAGTCTGGGAGGCGCCGCAAGAGCCCTTCTCCACCTGC 1198
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260

DB 1199 TCCTCCACCTCTGCGTAGTGCACTCTTCTTTGGACAGCGCCATCGTCATGATAGGCC 1258
QY 261 ProArgTyrGlyAsnProLysGlnGlnLysLysTyrLeuLeuPheHisSerLeuPhe 280
DB 1259 CCTAAGTCCCGGCATCTCTGAGGAGCAGCAAGAGTCTTTTCTATTTTACAGTTCTTTC 1318
QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
DB 1319 AACCCGATGCTAAACCCCTGATTTACAACTGAGGAATGTAGAGGTCAAGGTCCTGTG 1378
QY 301 LysArgValLeu 304
DB 1379 AGGAGAGCACTG 1390

RESULT 13
US-09-886-055-484
: Sequence 484, Application US/09886055
: Patent No. US20020132273A1
: GENERAL INFORMATION:
: APPLICANT: STYER, LUBERT
: APPLICANT: ZOZULYA, SERGEY
: TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
: FILE REFERENCE: 078003-0277150
: CURRENT APPLICATION NUMBER: US/09/886,055
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 522
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 484
: LENGTH: 933
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-886-055-484

Alignment Scores:
Pred. No.: 3,66e-97 Length: 933
Score: 991.00 Matches: 189
Percent Similarity: 77.42% Conservative: 51
Best Local Similarity: 60.97% Mismatches: 70
Query Match: 61.59% Indels: 0
DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-886-055-484 (1-933)

QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
DB 1 ATGCAAAAGCAATCAGACCTGGATCAGAGAAGTCATCTCTTGGGATTTCCAGGTGACCCA 60
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
DB 61 GCCTGAGTGTCTCTCTTTGGGTTTCTTCTGCTATTTCTACAGCTTAACCCCTGATGGGA 120
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
DB 121 AATGGGATTATCTCTGGGCTCATCTTACTTGGACTGTAGACTGTGACACACACCATGATGTC 180
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
DB 181 TTCTGTCAACACCTGGCCATGTGTGACATGTCTATAGCTCGAGTACTGTCCCTAAGATG 240
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
DB 241 CTAGCAATCTTGTGATGCACAAAAGTCATCTCTTGTGCTCTTGCATTACTTCAGACT 300
QY 101 PheLeuPheSerThrPheAlaValIleThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
DB 301 TTTTGTATTTGGCGCTTGTGCTATATACAGAGTGTCTGATTTTGGTGAATGATGTGCTATGAT 360
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140


```
Db 361 CGGTATGTGGCAATCTGTACACCCCTTGCAATACACCCCTCATTTATGAACCTGGAGAGTGTCC 420
QY 141 ILeThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 421 ACTGTCTGGCCTCAACTTGTCTGATATTAGCTTCTCTTGGCTGTGTCATATTTACT 480
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnPheIleTyrHisPhePheCysGluIle 180
Db 481 CTATATTCTGAGGCTGCCTTTTGTGGCCACACAAAGATCAACCACTTTTCTGTCAAAATC 540
QY 181 LeuAlaValLeuLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAla 200
Db 541 ATGTCCGATATTCAAATTGGCTGTGCTGACACTAGGCTCAACGAGGTGCTCTATTGTGCG 600
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 601 GGTTCGTGCCTTCACTTAGTGGGGCGCTCTGCCGTGTGCTGTCTCTACTTGCACATC 660
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 661 CTGGTGGCCATCTTGAGGATCCAGTCTGGGAGGGCGCCAGAAAGGCTTCTCTACCTGC 720
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 721 TCCTCCACCTCTGCTGTGGTGTCTTTCTTTGGCAGCGCCATTTGCATGTACATGCC 780
QY 261 ProArgTyrGlyAsnProLysGlnGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 781 CCCAAGTCAAGCCATTTCTCAAGAACGAGGAGAGATCCTTTCCCTGTTTACAGCCTTTTC 840
QY 281 AsnProMetLeuAsnProLeuIleLeuSerLeuArgAsnSerGluValLysAsnThrLeu 300
Db 841 AACCCGATCCTGAACCCCTCATCTACAGCCTTAGGAATGCAGAGTGAAAGGGGCTCTA 900
QY 301 LysArgValLeuGlyValGlnArgAlaLeu 310
Db 901 AAGAGAGTCCCTTGGAAACAGAGATCAATG 930

RESULT 14
US-09-886-055-472
; Sequence 472, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-055-472

Alignment Scores:
Pred. No.: 1,66e-92 Length: 930
Score: 947.50 Matches: 187
Percent Similarity: 74.68% Conservative: 43
Best Local Similarity: 60.71% Mismatches: 77
Query Match: 58.89% Indels: 1
DB: 10 Gaps: 1

US-09-898-586-24 (1-310) x US-09-886-055-472 (1-930)
QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1 ATGGAAGGCAACAAGACATGATCACAACATCACCCTTGCCCGGATTCACAGGTGGTCCA 60
```

```
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 61 GCACCTGGAGATTCCTCTGTGGACTTTTCGTGCTTCATACACTGCCTGCGGGG 120
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
Db 121 AATGGGGTCATCTTTGGGATTTATTCCTTGAGCTGTAAAGCTTCACACACCATGTAATTC 180
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 181 TTCCTCTACACACTGGCCCATTTGTGACATATCCTATGCTTCCAACTATGTCCCAAGATG 240
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
Db 241 CTGACGAATCTTTATGAACCGAAGACACCATCTCTTTTCCATGATGAATATGACAGCA 300
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValValMetSerTyrAsp 120
Db 301 TTCTTGTATTGGCTTTTGTCTCAGTAGAGTGTCTGATTTTGGTGGATGTCCTATGAT 360
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrrArgValCys 140
Db 361 CGCTATGGCGACATCTGCCACCCCTTAGCTTACATATTCCTCATGAGCTGCAGAGTGTGC 420
QY 141 IleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 421 ACTGTCTGTGGCTGTGCTTCTGCTGGTGTTCAGCTTCCTCTGCTGCTGTGCTTACTAGT 480
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 481 CTCATCCTGAGGCTGCTCCCTTCTGTGCGGCTCTCATGAAATCAACACAC--TTCTGTAAATC 537
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAla 200
Db 537 CTGTCTGTCTCAGTGTGGCTGTGCTGACACCTGGCTCAACGAGGTGCATCTTTGCA 597
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 598 GCCTGCTGTTCATCTGTGGGCGCACTCTGCCTGTGCTGTGCTGTCTACTTGGCGCATC 657
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 658 CTGGCCGCGCATCTGAGGATCCAGTCTGGGAGGGCGCCAGAAAGGCTTCTCCACCTGC 717
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 718 TCCTCCACCTTGTGGCTGTGGACTTCTTTGGCAGCGCCATTTGTCAAGTACATGGCC 777
QY 261 ProArgTyrGlyAsnProLysGlnGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 778 CCCAAGTCCCGCCATCTGAGGAGCAGCAAGATCTTCCCTGTTTACAGCCTTTTC 837
QY 281 AsnProMetLeuAsnProLeuIleLeuSerLeuArgAsnSerGluValLysAsnThrLeu 300
Db 838 AATCCAATGCTGAACCCCTGATATATAGCCTTAAGGAATGCAGAGGTCAAGGCGCCCTG 897
QY 301 LysArgValLeuGlyValGlnArg 308
Db 898 AGGAGGGCACTGAGGAGAGAGAGG 921

RESULT 15
US-09-886-055-486
; Sequence 486, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
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; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 486
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-886-055-486

Alignment Scores:
pred. No.: 1.25e-90 Length: 933
Score: 930.00 Matches: 181
Percent Similarity: 74.84% Conservative: 51
Best Local Similarity: 58.39% Mismatches: 78
Query Match: 57.80% Indels: 0
DB: 10 Gaps: 0

09-898-586-24 (1-310) x US-09-886-055-486 (1-933)

QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1 ATGGGGGACACCAATCAGCGGCTCAGATATTCATCCGTGGATTCCAGCTCAGTGTG 60
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 61 GAGATGGAAGTGTCTCTCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
Db 121 AATGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGGCGCACCCCATGTACTTC 180
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 181 TTCCTGTACACTTGGCCGTCATGTACATATATGCTTCCAGCAATTTGCTCAACATG 240
QY 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 241 CTGGAACACCTAGTGAACACAAAAAACTATCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 301 GCTTGTATTTGACTTTTGTGCTGTCAGAGTGTGCATGATTTTGGTGGATGTCTATGAC 360
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 361 AGATTGTGGGATCTGGCATCCCTGCATTTACACTGTCAATGAACCTGGAGAGTGTGC 420
QY 141 IleThrLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 421 ACAGTACTGGCTATTAATCTCTGGGCATGTGATTTTCCCTGGCCCTCATAAATCTAATT 480
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 481 CTCCTTCTAAGGCTGCCCTTCTGTGGGCCCCAGAGAGTGAACCACTCTTCGGTGAATT 540
QY 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 541 CTGTCTGTCTCAAACTGGCCTGTGACAGACACCTGGAATTAATGAATTTTGTCTTGTCT 600
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValIleValSerTyrMetCysIle 220
Db 601 GGTGGT 660
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 661 CTCCTTGGCCATCTGAAGATCCAGTCAAGAGGCGCAAAAAGCCCTTTTCCACCTGC 720
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 721 TCCTCCACCTCTGT 780
QY 261 ProArgTyrGlyAsnProLysGluGlnLysTyrLeuLeuLeuPheHisSerLeuPhe 280

Db 781 CCAGACAACACTCAACGACAGACAGACAGAAATTCACACCTGTGTGTGTGTGTGTGT 840
QY 281 AsnPrometLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
Db 841 AACCATTTGCTGAACCCCTCATCTTACAGCCTGCGGAATGCTCAAGTGAAGGCTGCTTGA 900
QY 301 LysArgValLeuGlyValGluArgAlaLeu 310
Db 901 TACAGAGCACTGCAGAAAAAGAGGACCATG 930

Search completed: January 2, 2003, 09:23:27
Job time : 814 secs

